

## SEQUENCE LISTING

- (1) GENERAL INFORMATION:
  - (iii) NUMBER OF SEQUENCES: 16
- (2) INFORMATION FOR SEQ ID NO: 1:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 963 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (iii) HYPOTHETICAL: N
  - (iv) ANTI-SENSE: N
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: Homo sapiens
  - (vii) IMMEDIATE SOURCE:
    - (B) CLONE: pTrimer(T0)
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 12..947
    - (D) OTHER INFORMATION:
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1

Hind III

BglII

AAGCTTACGTAAGATCTAACGGTCTCCCTGGCCCCATTGGGCCCCCTGGTCCTCG  
CGGTCGCACTGGTGATGCTGGTCCTGTTGGTCCCCCGGCCCTCCTGGACCTCCT  
GGTCCCCCTGGTCCTCCAGCGCTGGTTTCGACTTCAGCTTCCTGCCCCAGCCAC  
CTCAAGAGAAGGCTCACGATGGTGGCCGCTACTACCGGGCTGATGATGCCAATGT  
GGTTCGTGACCGTGACCTCGAGGTGGACACCACCCTCAAGAGCCTGAGCCAGCAG  
ATCGAGAACATCCGGAGCCCAGAGGGAAGCCGCAAGAACCCCGCCCGCACCTGCC  
GTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACCC  
CAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGT  
GAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCCAGAAGAACTGGTACATCA  
GCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGG  
ATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTGCCGATGTGGCCATCCAG  
CTGACCTTCCTGCGCCTGATGTCCACCGAGGCCTCCCAGAACATCACCTACCACT  
GCAAGAACAGCGTGGCCTACATGGACCAGCAGACTGGCAACCTCAAGAAGGCCCT  
GCTCCTCAAGGGCTCCAACGAGATCGAGATCCGCGCCGAGGGCAACAGCCGCTTC  
ACCTACAGCGTCACTGTCGATGGCTGCACGAGTCACACCGGAGCCTGGGGCAAGA  
CAGTGATTGAATACAAAACCACCAAGTCCTCCCGCCTGCCCATCATCGATGTGGC

CCCCTTGGACGTTGGTGCCCCAGACCAGGAATTCGGCTTCGACGTTGGCCCTGTC  
TGCTTCCTGTAAACTCCCTCCATCTAGA

Xba I

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2

1	RSNGLPGPIG PPGPRGRTGD AGPVGPPGPP GPPGPPGPPS AGFDFSFLPQ PPQEKAHDGG	60
61	RYRADDANV VRDRDLEVDV TLKLSQQIE NIRSPEGSRK NPARTCRDLK MCHSDWKSGE	120
121	YWIDPNQGCN LDAIKVFCNM ETGETCVYPT QPSVAQKNWY ISKNPKDKRH VWFGESMTDG	180
181	FQFEYGGQGS DPADVAIQLT FLRLMSTEAS QNITYHCKNS VAYMDQQTGN LKKALLLKGS	240
241	NEIEIRAEGN SRFTYSVTVD GCTSHTGAWG KTVIEYKTTK SSRLPIIDVA PLDVGAPDQE	300
301	FGFDVGPVCF L	

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

- (B) CLONE: pTrimer(T2)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 12..755
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3

Hind III

BglII

AAGCTTACGTAAGATCTGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCACCCT  
CAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCCAGAGGGAAGCCGCAAGAACCCCGCC

CGCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACC  
 CCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTG  
 CGTGTACCCCACTCAGCCCAGTGTGGCCCAGAAGAACTGGTACATCAGCAAGAACCCCAAGGAC  
 AAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGG  
 GCTCCGACCCTGCCGATGTGGCCATCCAGCTGACCTTCCTGCGCCTGATGTCCACCGAGGCCTC  
 CCAGAACATCACCTACCACTGCAAGAACAGCGTGGCCTACATGGACCAGCAGACTGGCAACCTC  
 AAGAAGGCCCTGCTCCTCAAGGGCTCCAACGAGATCGAGATCCGCGCCGAGGGCAACAGCCGCT  
 TCACCTACAGCGTCACTGTTCGATGGCTGCACGAGTCACACCGGAGCCTGGGGCAAGACAGTGAT  
 TGAATACAAAACCAAGTCCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGACGTTGGT  
 GCCCCAGACCAGGAATTCGGCTTCGACGTTGGCCCTGTCTGCTTCCTGT**TAA**ACTCCCTCCATCT  
AGA

Xba I

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4

1	RSDANVVRDR	DLEVDTTLKS	LSQQIENIRS	PEGSRKNPAP	TCRDLKMCHS	DWKSGEYWID	60
61	PNQGCNLDAI	KVFCNMETGE	TCVYPTQPSV	AQKNWYISK	PKDKRHVWFG	ESMTDGFQFE	120
121	YGGQGSDDPAD	VAIQLTFLRL	MSTEASQNIT	YHCKNSVAYM	DQQTGNLKKA	LLLKGSNEIE	180
181	IRAEGNSRFT	YSVTVDGCTS	HTGAWGKTVI	EYKTTKSSRL	PIIDVAPLDV	GAPDQEFQFD	240
241	VGPVCFL						

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

(B) CLONE: pTrimer/AP-T0  
(ix) FEATURE:  
    (A) NAME/KEY: CDS  
    (B) LOCATION: 12..2471  
    (D) OTHER INFORMATION:  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5

Hind III

AAGCTTCCTGC**ATG**CTGCTGCTGCTGCTGCTGCTGCTGGGCCTGAGGCTACAGCTCTCCCTG  
GGCATCATCCCAGTTGAGGAGGAGAACCCGGACTTCTGGAACCGCGAGGCAGCCGAGGC  
CCTGGGTGCCGCCAAGAAGCTGCAGCCTGCACAGACAGCCGCCAAGAACCTCATCATCT  
TCCTGGGCGATGGGATGGGGGTGTCTACGGTGACAGCTGCCAGGATCCTAAAAGGGCAG  
AAGAAGGACAACTGGGGCCTGAGATACCCCTGGCCATGGACCGCTTCCCATATGTGGC  
TCTGTCCAAGACATAACAATGTAGACAAACATGTGCCAGACAGTGGAGCCACAGCCACGG  
CCTACCTGTGCGGGGTCAAGGGCAACTTCCAGACCATTGGCTTGAGTGCAGCCGCCCGC  
TTTAACCAGTGCAACACGACACGCGGCAACGAGGTCATCTCCGTGATGAATCGGGCCAA  
GAAAGCAGGGAAAGTCAGTGGGAGTGGTAACCACCACACGAGTGCAGCACGCCTCGCCAG  
CCGGCACCTACGCCACACGGTGAACCGCAACTGGTACTCGGACGCCGACGTGCCTGCC  
TCGGCCCGCCAGGAGGGGTGCCAGGACATCGCTACGCAGCTCATCTCCAACATGGACAT  
TGACGTGATCCTAGGTGGAGGCCGAAAGTACATGTTTCCCATGGGAACCCCAGACCCTG  
AGTACCCAGATGACTACAGCCAAGGTGGGACCAGGCTGGACGGGAAGAATCTGGTGCAG  
GAATGGCTGGCGAAGCGCCAGGGTGCCCGGTATGTGTGGAACCGCACTGAGCTCATGCA  
GGCTTCCCTGGACCCGTCTGTGACCCATCTCATGGGTCTCTTTGAGCCTGGAGACATGA  
AATACGAGATCCACCGAGACTCCACACTGGACCCCTCCCTGATGGAGATGACAGAGGCT  
GCCCTGCGCCTGCTGAGCAGGAACCCCCGCGGCTTCTTCCCTCTTCGTGGAGGGTGGTCG  
CATCGACCATGGTCATCATGAAAGCAGGGCTTACCGGGCACTGACTGAGACGATCATGT  
TCGACGACGCCATTGAGAGGGCGGGCCAGCTCACCAGCGAGGAGGACACGCTGAGCCTC  
GTCACTGCCGACCACTCCACAGTCTTCTCCTTCGGAGGCTACCCCCTGCGAGGGAGCTC  
CATCTTCGGGCTGGCCCCCTGGCAAGGCCCGGGACAGGAAGGCCTACACGGTCCTCCTAT  
ACGGAAACGGTCCAGGCTATGTGCTCAAGGACGGCGCCCGGCCGGATGTTACCGAGAGC  
GAGAGCGGGAGCCCCGAGTATCGGCAGCAGTCAGCAGTGCCCCTGGACGAAGAGACCCA  
CGCAGGCGAGGACGTGGCGGTGTTGCGCGCGGGCCCGCAGGCGCACCTGGTTACGGCG  
TGCAGGAGCAGACCTTCATAGCGCACGTATGGCCTTCGCCGCCTGCCTGGAGCCCTAC  
ACCGCCTGCGACCTGGCGCCCCCGCCGGCACACCGACGCCGCGCACCCGGGTTCGGG  
AAGATCTAACGGTCTCCCTGGCCCCATTGGGCCCCCTGGTCCTCGCGGTGCGACTGGTG  
ATGCTGGTCCTGTTGGTCCCCCGGCCCTCCTGGACCTCCTGGTCCCCCTGGTCCTCCC  
AGCGCTGGTTTCGACTTCAGCTTCCTGCCCCAGCCACCTCAAGAGAAGGCTCACGATGG  
TGGCCGCTACTACCGGGCTGATGATGCCAATGTGGTTTCGTGACCGTGACCTCGAGGTGG  
ACACCACCTCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCCAGAGGGAAGC  
CGCAAGAACCCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAG  
TGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCT  
GCAACATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCCAAG  
AACTGGTACATCAGCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCAT

GACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTGCCGATGTGGCCA  
TCCAGCTGACCTTCCTGCGCCTGATGTCCACCGAGGCCTCCCAGAACATCACCTACCAC  
TGCAAGAACAGCGTGGCCTACATGGACCAGCAGACTGGCAACCTCAAGAAGGCCCTGCT  
CCTCAAGGGGCTCCAACGAGATCGAGATCCGCGCCGAGGGCAACAGCCGCTTCACCTACA  
GCGTCACTGTCGATGGCTGCACGAGTCACACCGGAGCCTGGGGCAAGACAGTGATTGAA  
TACAAAACCACCAAGTCCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGACGTTGG  
TGCCCCAGACCAGGAATTCGGCTTCGACGTTGGCCCTGTCTGCTTCCTGT**TAA**ACTCCCT  
CCATCTAGA

Xba I

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 819 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6

1	MLLLLLLLGL	RLQLSLGIIP	VEENPDFWN	REAAEALGAA	KKLQPAQTAA	KNLIIFLGDG	60
61	MGVSTVTAAR	ILKGQKKDKL	GPEIPLAMDR	FPYVALSKTY	NVDKHVPDSG	ATATAYLCGV	120
121	KGNFQTIGLS	AAARFNQCNT	TRGNEVISVM	NRAKKAGKSV	GVVTTTRVQH	ASPAGTYAHT	180
181	VNRNWYSAD	VPASARQEGC	QDIATQLISN	MDIDVILGGG	RKYMFPMGTP	DPEYPDDYSQ	240
241	GGTRLDGKNL	VQEWLAKRQG	ARYVWNRTTEL	MQASLDPSVT	HLMGLFEPGD	MKYEIHRDST	300
301	LDPSLMEMTE	AALRLLSRNP	RGFFLFVEGG	RIDHGHHSR	AYRALTETIM	FDDAIERAGQ	360
361	LTSEEDTSL	VTADHSHVFS	FGGYPLRGSS	IFGLAPGKAR	DRKAYTVLLY	GNGPGYVLKD	420
421	GARPDVTESE	SGSPEYRQOS	AVPLDEETHA	GEDVAVFARG	PQAHLVHGVQ	EQTFIAHVMA	480
481	FAACLEPYTA	CDLAPPAGTT	DAAHPGSGRS	NGLPGPIGPP	GPRGRTGDAG	PVGPPGPPGP	540
541	PGPPGPPSAG	FDFSFLPQPP	QEKAHDGGRY	YRADDANVVR	DRDLEVDTTL	KSLSQQIENI	600
601	RSPEGSRKNP	ARTCRDLKMC	HSDWKSGEYW	IDPNQGCNLD	AIKVFCNMET	GETCVYPTQP	660
661	SVAQKNWYIS	KNPKDKRHVW	FGESMTDGFQ	FEYGGQGSDF	ADVAIQLTFL	RLMSTEASQN	720
721	ITYHCKNSVA	YMDQQTGNLK	KALLLKGSNE	IEIRAEGNSR	FTYSVTVDGC	TSHTGAWGKT	780
781	VIEYKTTKSS	RLPIIDVAPL	DVGAPDQEFQ	FDVGPVCFL			

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2294 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

(B) CLONE: pTrimer/AP-T2

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 12..2278

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7

Hind III

AAGCTTCCTGC**ATG**CTGCTGCTGCTGCTGCTGCTGCTGGGCCTGAGGCTACAGCTCTCCCTG  
GGCATCATCCCAGTTGAGGAGGAGAACCCGGACTTCTGGAACCGCGAGGCAGCCGAGGC  
CCTGGGTGCCGCAAGAAGCTGCAGCCTGCACAGACAGCCGCCAAGAACCTCATCATCT  
TCCTGGGCGATGGGATGGGGGTGTCTACGGTGACAGCTGCCAGGATCCTAAAAGGGCAG  
AAGAAGGACAACTGGGGCCTGAGATACCCCTGGCCATGGACCGCTTCCCATATGTGGC  
TCTGTCCAAGACATACAATGTAGACAAACATGTGCCAGACAGTGGAGCCACAGCCACGG  
CCTACCTGTGCGGGGTCAAGGGCAACTTCCAGACCATTGGCTTGAGTGCAGCCGCCCGC  
TTTAACCAAGTGCAACACGACACGCGGCAACGAGGTCATCTCCGTGATGAATCGGGCCAA  
GAAAGCAGGGAAGTCAGTGGGAGTGGTAACCACCACACGAGTGCAGCACGCCTCGCCAG  
CCGGCACCTACGCCACACGGTGAACCGCAACTGGTACTCGGACGCCGACGTGCCTGCC  
TCGGCCCCGCCAGGAGGGGTGCCAGGACATCGCTACGCAGCTCATCTCCAACATGGACAT  
TGACGTGATCCTAGGTGGAGGCCGAAAGTACATGTTTCCCATGGGAACCCCAGACCCTG  
AGTACCCAGATGACTACAGCCAAGGTGGGACCAGGCTGGACGGGAAGAATCTGGTGCAG  
GAATGGCTGGCGAAGCGCCAGGGTGCCCGGTATGTGTGGAACCGCACTGAGCTCATGCA  
GGCTTCCCTGGACCCGTCTGTGACCCATCTCATGGGTCTCTTTGAGCCTGGAGACATGA  
AATACGAGATCCACCGAGACTCCACACTGGACCCCTCCCTGATGGAGATGACAGAGGCT  
GCCCTGCGCCTGCTGAGCAGGAACCCCCGCGGCTTCTTCCTCTTCGTGGAGGGTGGTCG  
CATCGACCATGGTCATCATGAAAGCAGGGCTTACCGGGCACTGACTGAGACGATCATGT  
TCGACGACGCCATTGAGAGGGCGGGCCAGCTCACCAGCGAGGAGGACACGCTGAGCCTC  
GTCACTGCCGACCACTCCCACGTCTTCTCCTTCGGAGGCTACCCCCTGCGAGGGAGCTC  
CATCTTCGGGCTGGCCCCTGGCAAGGCCCGGGACAGGAAGGCCTACACGGTCCTCCTAT  
ACGGAAACGGTCCAGGCTATGTGCTCAAGGACGGCGCCCGGCGGATGTTACCGAGAGC  
GAGAGCGGGAGCCCCGAGTATCGGCAGCAGTCAGCAGTGCCCCTGGACGAAGAGACCCA  
CGCAGGCGAGGACGTGGCGGTGTTGCGCGCGCGGCCCGCAGGCGCACCTGGTTCACGGCG  
TGCAGGAGCAGACCTTCATAGCGCACGTGATGGCCTTCGCCGCTGCCTGGAGCCCTAC  
ACCGCCTGCGACCTGGCGCCCCCGCCGGCACCAACCGACGCCGCGCACCCGGGTTCGGG  
AGATCTGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCACCCTCAAGAG  
CCTGAGCCAGCAGATCGAGAACATCCGGAGCCCAGAGGGAAGCCGCAAGAACCCCGCCC  
GCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTACTGGATT  
GACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGG  
TGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCCAGAAGAAGTGGTACATCAGCA  
AGAACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAG  
TTCGAGTATGGCGGCCAGGGCTCCGACCCTGCCGATGTGGCCATCCAGCTGACCTTCCT

GCGCCTGATGTCCACCGAGGCCTCCCAGAACATCACCTACCACTGCAAGAACAGCGTGG  
 CCTACATGGACCAGCAGACTGGCAACCTCAAGAAGGCCCTGCTCCTCAAGGGCTCCAAC  
 GAGATCGAGATCCGCGCCGAGGGCAACAGCCGCTTACCTACAGCGTCACTGTTCGATGG  
 CTGCACGAGTCACACCGGAGCCTGGGGCAAGACAGTGATTGAATACAAAACCAAGT  
 CCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGACGTTGGTGCCCCAGACCAGGAA  
 TTCGGCTTCGACGTTGGCCCTGTCTGCTTCCTG**TAA**ACTCCCTCCATCTAGA

Xba I

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 755 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8

1	MLLLLLLLGL	RLQLSLGIIP	VEEENPDFWN	REAAEALGAA	KKLQPAQTAA	KNLFIFLGDG	60
61	MGVSTVTAAR	ILKGQKKDKL	GPEIPLAMDR	FPYVALSKTY	NVDKHVPDSG	ATATAYLCGV	120
121	KGNFQTIGLS	AAARFNQCNT	TRGNEVISVM	NRACKAGKSV	GVVTTTRVQH	ASPAGTYAHT	180
181	VNRNWYSAD	VPASARQEGC	QDIATQLISN	MDIDVILGGG	RKYMFPMTGP	DPEYPDDYSQ	240
241	GGTRLDGKNL	VQEWLAKRQG	ARYVWNRTSL	MQASLDPSVT	HLMGLFEPGD	MKYEIHRDST	300
301	LDPSLMEMTE	AALRLLSRNP	RGFFLFVEGG	RIDHGHHSR	AYRALTETIM	FDDAIERAGQ	360
361	LTSEEDTLSL	VTADHSHVFS	FGGYPLRGSS	IFGLAPGKAR	DRKAYTVLLY	GNGPGYVLKD	420
421	GARPDVTESE	SGSPEYRQOS	AVPLDEETHA	GEDVAVFARG	PQAHLVHGVQ	EQTFAHVMA	480
481	FAACLEPYTA	CDLAPPAGTT	DAAHPGSGRS	DANVVRDRDL	EVDTTLKSL	QQIENIRSP	540
541	GSRKNPARTC	RDLKMCHSDW	KSGEYWDPN	QGCNLDAIKV	FCNMETGETC	VYPTQPSVAQ	600
601	KNWYISKPNK	DKRHVWFGE	MTDGFQFEYG	GQGSDDADVA	IQLTFLRLMS	TEASQNITYH	660
661	CKNSVAYMDQ	QTGNLKKALL	LKGSNEIEIR	AEGNSRFTYS	VTVDGCTSHT	GAWGKTVIEY	720
721	KTTKSSRLPI	IDVAPLDVGA	PDQEFQFDVG	PVCFL			

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1734 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

- (vii) IMMEDIATE SOURCE:  
    (B) CLONE: pTrimer/sTNFR1I-T0  
(ix) FEATURE:  
    (A) NAME/KEY: CDS  
    (B) LOCATION: 18..1718  
    (D) OTHER INFORMATION:  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9

Bam HI

GGATCCCGCCCGCACCC**ATGG**CGCCCGTCGCCGTCTGGGCCGCGCTGGCCGTCGGACTGGAGCT  
CTGGGCTGCGGCGCACGCCTTGCCCCGCCAGGTGGCATTACACCCTACGCCCCGGAGCCCGGG  
AGCACATGCCGGCTCAGAGAATACTATGACCAGACAGCTCAGATGTGCTGCAGCAAATGCTCGC  
CGGGCCAACATGCAAAAGTCTTCTGTACCAAGACCTCGGACACCGTGTGTGACTCCTGTGAGGA  
CAGCACATACACCCAGCTCTGGAAGTGGGTTCCCGAGTGCTTGAGCTGTGGCTCCCGCTGTAGC  
TCTGACCAGGTGGAACTCAAGCCTGCACTCGGGAACAGAACCGCATCTGCACCTGCAGGCCCG  
GCTGGTACTGCGCGCTGAGCAAGCAGGAGGGGTGCCGGCTGTGCGCGCCGCTGCGCAAGTGCCG  
CCCGGGCTTCGGCGTGCCAGACCAGGAAGTGAACATCAGACGTGGTGTGCAAGCCCTGTGCC  
CCGGGGACGTTCTCCAACACGACTTCATCCACGGATATTTGCAGGCCCCACCAGATCTGTAACG  
TGGTGGCCATCCCTGGGAATGCAAGCATGGATGCAGTCTGCACGTCCACGTCCCCCACCAGGAG  
TATGGCCCCAGGGGACAGTACACTTACCCACAGCAGTGTCACACGATCCCAACACACGCAGCCA  
ACTCCAGAACCCAGCACTGCTCCAAGCACCTCCTTCCTGCTCCCAATGGGCCCCAGCCCCCAG  
CTGAAGGGAGCACTGGATCTAACGGTCTCCCTGGCCCCATTGGGCCCCCTGGTCCTCGCGG  
TCGCACTGGTGATGCTGGTCCTGTTGGTCCCCCGGCCCTCCTGGACCTCCTGGTCCCC  
CTGGTCCTCCCAGCGCTGGTTTCGACTTCAGCTTCCTGCCCCAGCCACCTCAAGAGAAG  
GCTCACGATGGTGGCCGCTACTACCGGGCTGATGATGCCAATGTGGTTCGTGACCGTGA  
CCTCGAGGTGGACACCACCCTCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCC  
CAGAGGGAAGCCGCAAGAACCCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCT  
GACTGGAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCAT  
CAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTG  
TGGCCCAGAAGAACTGGTACATCAGCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTC  
GGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTGC  
CGATGTGGCCATCCAGCTGACCTTCCTGCGCCTGATGTCCACCGAGGCCTCCCAGAACA  
TCACCTACCACTGCAAGAACAGCGTGGCCTACATGGACCAGCAGACTGGCAACCTCAAG  
AAGGCCCTGCTCCTCAAGGGCTCCAACGAGATCGAGATCCGCGCCGAGGGCAACAGCCG  
CTTCACCTACAGCGTCACTGTGATGGCTGCACGAGTCACACCGGAGCCTGGGGCAAGA  
CAGTGATTGAATACAAAACCAAGTCCTCCCGCCTGCCCATCATCGATGTGGCCCCC  
TTGGACGTTGGTGCCCCAGACCAGGAATTCGGCTTCGACGTTGGCCCTGTCTGCTTCCT  
**GTA**AACTCCCTCCATCTAGA

Xba I

- (2) INFORMATION FOR SEQ ID NO: 10:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 566 amino acids  
        (B) TYPE: amino acid



(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: protein  
(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10

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1 MAPVAVWAAL AVGLELWAAA HALPAQVAFT PYAPEPGSTC RLREYYDQTA QMCCSKCSPG    60
61 QHAKVFCTKT SDTVCDSCED STYTQLWNWV PECLSCGSRG SSDQVETQAC TREQNRICTC   120
121 RPGWYCALSK QEGCRLCAPL RKCRPGFGVA RPTGTSADV CKPCAPGTFS NTTSSDICTR   180
181 PHQICNVVAI PGNASMDAVC TSTSPTRSMA PGAVHLPQPV STRSQHTQPT PEPSTAPSTS   240
241 FLLPMGPSPP AEGSTGSNGL PGPIGPPGPR GRTGDAGPVG PPGPPGPPGP PGPPSAGFDF   300
301 SFLPQPPQEK AHDGGYYRA DDANVVRDRD LEVDTTLSL SQQIENIRSP EGSRKNPART   360
361 CRDLKMCHSD WKSGEYWIDP NQGCNLDAIK VFCNMETGET CVYPTQPSVA QKNWYISKNP   420
421 KDKRHWVFGE SMTDGFQFEY GGQGSDDPADV AIQLTFLRLM STEASQNTY HCKNSVAYMD   480
481 QQTGNLKKAL LLKGSNEIEI RAEGNSRFTY SVTVDGCTSH TGAWGKTIVIE YKTTKSSRLP   540
541 IIDVAPLDVG APDQEFQFDV GPVCFL

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(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1542 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(iii) HYPOTHETICAL: N  
(iv) ANTI-SENSE: N  
(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens  
(vii) IMMEDIATE SOURCE:  
(B) CLONE: pTrimer/sTNFR1I-T2  
(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 18..1526  
(D) OTHER INFORMATION:  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11

Bam HI

GGATCCCGCCCGCACCC**ATG**GGCGCCCGTCGCCGTCTGGGCGCGCTGGCCGTCGGACTGGAGCT  
CTGGGCTGCGGCGCACGCCTTGCCCGCCAGGTGGCATTTACACCCTACGCCCCGGAGCCCGGG  
AGCACATGCCGGCTCAGAGAATACTATGACCAGACAGCTCAGATGTGCTGCAGCAAATGCTCGC  
CGGGCCAACATGCAAAAGTCTTCTGTACCAAGACCTCGGACACCGTGTGTGACTCCTGTGAGGA  
CAGCACATACCCAGCTCTGGAAGTGGGTTCCCGAGTGCTTGAGCTGTGGCTCCCGCTGTAGC  
TCTGACCAGGTGGAACTCAAGCCTGCACTCGGGAACAGAACCGCATCTGCACCTGCAGGCCCG

GCTGGTACTGCGCGCTGAGCAAGCAGGAGGGGTGCCGGCTGTGCGCGCCGCTGCGCAAGTGCCG  
 CCCGGGCTTCGGCGTGGCCAGACCAGGAAGTGAACATCAGACGTGGTGTGCAAGCCCTGTGCC  
 CCGGGGACGTTCTCCAACACGACTTCATCCACGGATATTTGCAGGCCCCACCAGATCTGTAACG  
 TGGTGGCCATCCCTGGGAATGCAAGCATGGATGCAGTCTGCACGTCCACGTCCCCCACC GGAG  
 TATGGCCCCAGGGGCAGTACACTTACCCCAGCCAGTGTCCACACGATCCCAACACACGCAGCCA  
 ACTCCAGAACCCAGCACTGCTCCAAGCACCTCCTTCCTGCTCCCAATGGGCCCCAGCCCCCAG  
 CTGAAGGGAGCACTGGATCTGATGCCAATGTGGTTCTGTGACCGTGACCTCGAGGTGGACAC  
 CACCCTCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCCAGAGGGAAGCCGCA  
 AGAACCCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGA  
 GAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAA  
 CATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCCAGAAGAAGT  
 GGTACATCAGCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACC  
 GATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTGCCGATGTGGCCATCCA  
 GCTGACCTTCCTGCGCCTGATGTCCACCGAGGCCTCCAGAACATCACCTACCACTGCA  
 AGAACAGCGTGGCCTACATGGACCAGCAGACTGGCAACCTCAAGAAGGCCCTGCTCCTC  
 AAGGGCTCCAACGAGATCGAGATCCGCGCCGAGGGCAACAGCCGCTTCACCTACAGCGT  
 CACTGTGATGGCTGCACGAGTCAACCCGAGCCTGGGGCAAGACAGTGATTGAATACA  
 AAACCACCAAGTCCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGACGTTGGTGCC  
 CCAGACCAGGAATTCGGCTTCGACGTTGGCCCTGTCTGCTTCCTG**TAA**ACTCCCTCCAT  
 CTAGA

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(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12

1	MAPVAVWAAL	AVGLELWAAA	HALPAQVAFT	PYAPEPGSTC	RLREYYDQTA	QMCCSKCSPG	60
61	QHAKVFCTKT	SDTVCDSCED	STYTQLWNWV	PECLSCGSR	SSDQVETQAC	TREQNRICTC	120
121	RPGWYCALSK	QEGCRLCAPL	RKCRPGFGVA	RPGTETSDV	CKPCAPGTFS	NTTSSTDICR	180
181	PHQICNVVAI	PGNASMDAVC	TSTSPTRSMA	PGAVHLPQPV	STRSQHTQPT	PEPSTAPSTS	240
241	FLLPMGPSP	AEGSTSDAN	VVRDRDLEVD	TTLKSLSQQI	ENIRSPEGS	KNPARTCRDL	300
301	KMCHSDWKSG	EYWIDPNQGC	NLDAIKVFCN	METGETCVYP	TQPSVAQKNW	YISKNPDKDR	360
361	HVWFGESEMTD	GFQFEYGGQG	SDPADVAIQ	TFLRLMSTEA	SNITYHCKN	SVAYMDQQTG	420
421	NLKKALLLKG	SNEIEIRAEG	NSRFTYSVT	DGCTSHTGAW	GKTVIEYKTT	KSSRLPIIDV	480
481	APLDVGAPDQ	EFGFDVGPVC	FL				

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2139 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: N
- (iv) ANTI-SENSE: N
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: pTrimer/sCD4-T0
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 24..2123
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13

Hind III

AAGCTTCCCTCGGCAAGGCCACA**ATGA**ACCGGGGAGTCCCTTTTAGGCACTTGCTTCTG  
GTGCTGCAACTGGCGCTCCTCCCAGCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGCAA  
AAAAGGGGATACAGTGGAAGTACCTGTACAGCTTCCCAGAAGAAGAGCATACAATTCC  
ACTGGAAAACTCCAACCAGATAAAGATTCTGGGAAATCAGGGGCTCCTTCTTAATAAAA  
GGTCCATCCAAGCTGAATGATCGCGCTGACTCAAGAAGAAGCCTTTGGGACCAAGGAAA  
CTTTCCCTGATCATCAAGAATCTTAAGATAGAAGACTCAGATACTTACATCTGTGAAG  
TGGAGGACCAGAAGGAGGAGGTGCAATTGCTAGTGTTTCGGATTGACTGCCAACTCTGAC  
ACCCACCTGCTTCAGGGGCAGAGCCTGACCCTGACCCTTGGAGAGCCCCCTGGTAGTAG  
CCCCTCAGTGCAATGTAGGAGTCCAAGGGGTAAAAACATACAGGGGGGGAAGACCCTCT  
CCGTGTCTCAGCTGGAGCTCCAGGATAGTGGCACCTGGACATGCACTGTCTTGCAGAAC  
CAGAAGAAGGTGGAGTTCAAAATAGACATCGTGGTGCTAGCTTTCCAGAAGGCCTCCAG  
CATAGTCTATAAGAAAGAGGGGGAACAGGTGGAGTTCTCCTTCCCACTCGCCTTTACAG  
TTGAAAAGCTGACGGGCAGTGGCGAGCTGTGGTGGCAGGCGGAGAGGGCTTCCTCCTCC  
AAGTCTTGATCACCTTTGACCTGAAGAACAAGGAAGTGTCTGTAAAACGGGTACCCA  
GGACCCTAAGCTCCAGATGGGCAAGAAGCTCCCGCTCCACCTCACCTGCCCCAGGCCT  
TGCCTCAGTATGCTGGCTCTGGAAACCTCACCTGGCCCTTGAAGCGAAAACAGGAAAG  
TTGCATCAGGAAGTGAACCTGGTGGTGATGAGAGCCACTCAGCTCCAGAAAAATTTGAC  
CTGTGAGGTGTGGGGACCCACCTCCCCTAAGCTGATGCTGAGCTTGAACTGGAGAACA  
AGGAGGCAAAGGTCTCGAAGCGGGAGAAGGCGGTGTGGGTGCTGAACCCTGAGGCGGGG  
ATGTGGCAGTGTCTGCTGAGTGACTCGGGACAGGTCCTGCTGGAATCCAACATCAAGGT  
TCTGCCCAGATCTAACGGTCTCCCTGGCCCCATTGGGCCCCCTGGTCCTCGCGGTCGCA  
CTGGTGATGCTGGTCTGTGGTCCCCCGGCCCTCCTGGACCTCCTGGTCCCCCTGGT  
CCTCCCAGCGCTGGTTTCGACTTCAGCTTCCTGCCCCAGCCACCTCAAGAGAAGGCTCA  
CGATGGTGGCCGCTACTACCGGGCTGATGATGCCAATGTGGTTCGTGACCGTGACCTCG

AGGTGGACACCACCCTCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCCAGAG  
GGAAGCCGCAAGAACCCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTG  
GAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAG  
TCTTCTGCAACATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCC  
CAGAAGAACTGGTACATCAGCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGA  
GAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTGCCGATG  
TGGCCATCCAGCTGACCTTCCTGCGCCTGATGTCCACCGAGGCCTCCCAGAACATCACC  
TACCACTGCAAGAACAGCGTGCCCTACATGGACCAGCAGACTGGCAACCTCAAGAAGGC  
CCTGCTCCTCAAGGGCTCCAACGAGATCGAGATCCGCGCCGAGGGCAACAGCCGCTTCA  
CCTACAGCGTCACTGTCGATGGCTGCACGAGTCACACCGGAGCCTGGGGCAAGACAGTG  
ATTGAATACAAAACCAAGTCCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGA  
CGTTGGTGCCCCAGACCAGGAATTCGGCTTCGACGTTGGCCCTGTCTGCTTCCTG**TAAA**  
CTCCCTCCATCTAGA

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(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 699 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14

1	MNRGVFPRHL	LLVLQLALLP	AATQGKKVVL	GKKGDTVELT	CTASQKKSIQ	FWKNSNQIK	60
61	ILGNQGSFLT	KGPSKLNDR	DSRRSLWDQG	NFPLIIKNLK	IEDSDTYICE	VEDQKEEVQL	120
121	LVFGLTANS	THLLQGQSLT	LTLESPPGSS	PSVQCRSPRG	KNIQGGKTLS	VSQLELQDSG	180
181	TWTCTVLQNQ	KKVEFKIDIV	VLAFAQASSI	VYKKEGEQVE	FSFPLAFTVE	KLTGSGELWW	240
241	QAERASSSKS	WITFDLKNKE	VSVKRVTDQP	KLQMGKKLPL	HLTLPQALPQ	YAGSGNLTLA	300
301	LEAKTGKLHQ	EVNLVVMRAT	QLQKNLTCEV	WGPTSPKLML	SLKLENKEAK	VSKREKAVWV	360
361	LNPEAGMWQC	LLSDSGQVLL	ESNIKVLPRS	<u>NGLPGPIGPP</u>	<u>GPRGRTGDAG</u>	<u>PVGPPGPPGP</u>	420
421	<u>PGPPGPPSAG</u>	<u>FDFSFLPQPP</u>	<u>QEKAHDGGRY</u>	<u>YRADDANVVR</u>	<u>DRDLEVDTTL</u>	<u>KSLSQQIENI</u>	480
481	RSPEGSRKNP	ARTCRDLKMC	HSDWKSGEYW	IDPNQGCNLD	AIKVFCNMET	GETCVYPTQP	540
541	SVAQKNWYIS	KNPKDKRHVW	FGESMTDGFQ	FEYGGQGS DP	ADVAIQLTFL	RLMSTEASQN	600
601	ITYHCKNSVA	YMDQQTGNLK	KALLLKGSNE	IEIRAEGNSR	FTYSVTVDGC	TSHTGAWGKT	660
661	VIEYKTTKSS	RLPIIDVAPL	DVGAPDQEF	FDVGPVCF			

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1947 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(iii) HYPOTHETICAL: N  
(iv) ANTI-SENSE: N  
(vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo sapiens  
  
(vii) IMMEDIATE SOURCE:  
    (B) CLONE: pTrimer/sCD4-T2  
(ix) FEATURE:  
    (A) NAME/KEY: CDS  
    (B) LOCATION: 24..1931  
    (D) OTHER INFORMATION:  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15

Hind III

AAGCTTCCCTCGGCAAGGCCACA**ATGA**ACCGGGGAGTCCCTTTTAGGCACTTGCTTCTG  
GTGCTGCAACTGGCGCTCCTCCCAGCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGCAA  
AAAAGGGGATACAGTGGAAGTACCTGTACAGCTTCCAGAAGAAGAGCATACAATTCC  
ACTGGAAAACTCCAACCAGATAAAGATTCTGGGAAATCAGGGCTCCTTCTTAATAAAA  
GGTCCATCCAAGCTGAATGATCGCGCTGACTCAAGAAGAAGCCTTTGGGACCAAGGAAA  
CTTTCCCTGATCATCAAGAATCTTAAGATAGAAGACTCAGATACTTACATCTGTGAAG  
TGGAGGACCAGAAGGAGGAGGTGCAATTGCTAGTGTTCTGGATTGACTGCCAACTCTGAC  
ACCCACCTGCTTCAGGGGCAGAGCCTGACCCTGACCTTGGAGAGCCCCCTGGTAGTAG  
CCCCTCAGTGCAATGTAGGAGTCCAAGGGGTAAAAACATACAGGGGGGGAAGACCCTCT  
CCGTGTCTCAGCTGGAGCTCCAGGATAGTGGCACCTGGACATGCACTGTCTTGACAGAAC  
CAGAAGAAGGTGGAGTTCAAAATAGACATCGTGGTGCTAGCTTTCCAGAAGGCCTCCAG  
CATAGTCTATAAGAAAGAGGGGGAACAGGTGGAGTTCTCCTTCCCCTCGCCTTTACAG  
TTGAAAAGCTGACGGGCAGTGGCGAGCTGTGGTGGCAGGCGGAGAGGGCTTCCTCCTCC  
AAGTCTTGGATCACCTTTGACCTGAAGAACAAGGAAGTGTCTGTAAAACGGGTACCCA  
GGACCCTAAGCTCCAGATGGGCAAGAAGCTCCCGCTCCACCTCACCTGCCCCAGGCCT  
TGCCTCAGTATGCTGGCTCTGGAAACCTCACCTGGCCCTTGAAGCGAAAACAGGAAAG  
TTGCATCAGGAAGTGAACCTGGTGGTGTGAGAGCCACTCAGCTCCAGAAAAATTTGAC  
CTGTGAGGTGTGGGGACCCACCTCCCCTAAGCTGATGCTGAGCTTGAAACTGGAGAACA  
AGGAGGCAAAGGTCTCGAAGCGGGAGAAGGCGGTGTGGGTGCTGAACCCTGAGGCGGGG  
ATGTGGCAGTGTCTGCTGAGTGACTCGGGACAGGTCTGCTGGAATCCAACATCAAGGT  
TCTGCCCAGATCTGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCACCC  
TCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCCAGAGGGAAGCCGCAAGAAC  
CCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTA  
CTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGG  
AGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAAGTGTGGCCAGAGAAGTGGTAC  
ATCAGCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGG  
ATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTGCCGATGTGGCCATCCAGCTGA

CCTTCCTGCGCCTGATGTCCACCGAGGCTCCCAGAACATCACCTACCACTGCAAGAAC  
 AGCGTGGCCTACATGGACCAGCAGACTGGCAACCTCAAGAAGGCCCTGCTCCTCAAGGG  
 CTCCAACGAGATCGAGATCCGCGCCGAGGGCAACAGCCGCTTCACCTACAGCGTCACTG  
 TCGATGGCTGCACGAGTCACACCGGAGCCTGGGGCAAGACAGTGATTGAATACAAAACC  
 ACCAAGTCCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGACGTTGGTGCCCCAGA  
 CCAGGAATTCGGCTTCGACGTTGGCCCTGTCTGCTTCCTG**TAA**ACTCCCTCCATCTAGA

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(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 635 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16

1	MNRGVPFRHL	LLVLQLALLP	AATQGKKVVL	GKKGDTVELT	CTASQKKSQ	FWKNSNQIK	60
61	ILGNQGSFLT	KGPSKLNDRA	DSRRSLWDQG	NFPLIIKNLK	IEDSDTYICE	VEDQKEEVQL	120
121	LVFGLTANS	THLLQGQSLT	LTLESPPGSS	PSVQCRSPRG	KNIQGGKTLS	VSQLELQDSG	180
181	TWTCTVLQ	NQKKVEFKIDIV	VLAFAQASSI	VYKKEGEQVE	FSFPLAFTVE	KLTGSGELWW	240
241	QAERASSSKS	WITFDLKNKE	VSVKRVTDQP	KLQMGKKLPL	HLTLPQALPQ	YAGSGNLTLA	300
301	LEAKTGKLHQ	EVNLVVMRAT	QLQKNLTCEV	WGPTSPKLML	SLKLENKEAK	VSKREKAVVW	360
361	LNPEAGMWQC	LLSDSGQVLL	ESNIKVLPR <b>S</b>	DANVVRDRDL	EVDTTLKSL	QQIENIRSPE	420
421	GSRKNPARTC	RDLKMCHSDW	KSGEYWIDPN	QGCNLDAIKV	FCNMETGETC	VYPTQPSVAQ	480
481	KNWYISKNP	KDKRHVWFGES	MTDGFQFEYG	GQGSPPADVA	IQLTFLRLMS	TEASQNITYH	540
541	CKNSVAYMDQ	QTGNLKKALL	LKGSNEIEIR	AEGNSRFTYS	VTVDGCTSHT	GAWGKTVIEY	600
601	KTTKSSRLPI	IDVAPLDVGA	PDQEFQFDVG	PVCFL			